

CRF Errors Corrected by the STIC System Branch

Serial Number: 09/903,377

CRF Processing Date: 2/6/2002  
 Edited by: Ar  
 Verified by: Ar (STIC staff)

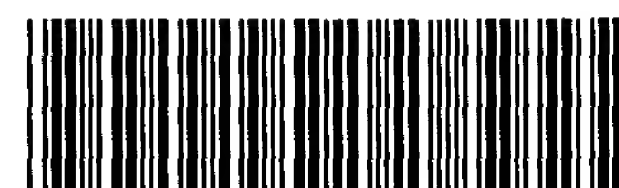
**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

# 6



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/903,377

DATE: 02/06/2002

TIME: 08:10:32

Input Set : N:\jumbos\903377.txt

Output Set: N:\CRF3\02062002\I903377.raw

4 <110> APPLICANT: Allen, Keith D.  
6 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE  
7 RECEPTOR 9A GENE DISRUPTIONS  
10 <130> FILE REFERENCE: R-365  
12 <140> CURRENT APPLICATION NUMBER: US 09/903,377  
13 <141> CURRENT FILING DATE: 2001-07-10  
15 <150> PRIOR APPLICATION NUMBER: US 60/217,255  
16 <151> PRIOR FILING DATE: 2000-07-10  
18 <150> PRIOR APPLICATION NUMBER: US 60/221,483  
19 <151> PRIOR FILING DATE: 2000-07-27  
21 <150> PRIOR APPLICATION NUMBER: US 60/262,113  
22 <151> PRIOR FILING DATE: 2001-01-16  
24 <160> NUMBER OF SEQ ID NOS: 4  
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 2577  
30 <212> TYPE: DNA  
31 <213> ORGANISM: Artificial Sequence  
33 <220> FEATURE:  
34 <223> OTHER INFORMATION: Targeting vector  
36 <400> SEQUENCE: 1  
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38 gctgatgact atggctctga atccacatct tccatggaag actacgttaa cttcaacttc 120  
39 actgacttct actgtgagaa aaacaatgtc aggcagtttg cgagccattt cctcccaccc 180  
40 ttgtactggc tcgtgttcat cgtgggtgcc ttgggcaaca gtcttggtat ccttgtctac 240  
41 tggtagtgca caagagtga gaccatgacc gacatgttcc ttttgaattt ggcaattgct 300  
42 gacctcctct ttcttgtcac tcttcccttc tgggccattg ctgctgctga ccagtggag 360  
43 ttccagacct tcatgtgcaa ggtgggtcaac agcatgtaca agatgaactt ctacagctgt 420  
44 gtgttgctga tcatgtgcat cagcgtggac aggtacattg ccattgcccc ggccatgaga 480  
45 gcacatactt ggagggagaa aaggcttttg tacagcaaaa tggtttgctt taccatctgg 540  
46 gtattggcag ctgctctctg catcccagaa atcttataca gccaaatcaa ggaggaatcc 600  
47 ggcattgcta tctgcacat ggtttaccct agcagtgaga gcaccaaact gaagtcagct 660  
48 gtcttgacct tgaaggatcat tctgggttcc ttccttccct tcgtgggtcat ggcttgctgc 720  
49 tataccatca tcattcacac cctgatacaa gccaagaagt cttccaagca caaagcccta 780  
50 aaagtgaaca tcaactgtcct gaccgtcttt gtcttgtctc agtttcccta caactgcatt 840  
51 ttgttggtgc agaccattga cgcctatgcc atgttcatct ccaactgtgc cgtttccacc 900  
52 aacattgaca tctgcttcca ggtaaccag accatcgctt tcttccacag ttgcctgaac 960  
53 cctgttctct atgtttttgt gggtagagaa ttccgcccgg atctcgtgaa aaccctgaag 1020  
54 aacttggtgt gcatcagcca ggcccagtg gtttcattta caaggagaga gggagcttg 1080  
55 aagctgtcgt ctatgttgct ggagacaacc tcaggagcac tctccctctg aggggtcttc 1140  
56 tctgaggtgc atggttcttt tggaagaaat gagaaataca tgaaacagtt tccccactga 1200  
57 tgggaccaga gagagtgaag gagaaaagaa aactcagaaa gggatgaatc tgaactatat 1260  
58 gattacttgt agtcagaatt tgccaaagca aatatttcaa aatcaactga ctagtgcagg 1320

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59 aggetgttga ttggtcttg actgtgatgc cgcgaattct caaaggagga ctaaggaccg 1380
60 gcactgtgga gcaccctggc tttgccactc gccggagcat caatgccgct gcctctggag 1440
61 gagcccttgg attttctcca tgcactgtga acttctgtgg cttcagttct catgctgcct 1500
62 cttccaaaag gggacacaga agcactggct gctgctacag accgcaaaag cagaaagttt 1560
63 cgtgaaaatg tccatctttg ggaaattttc taccctgctc ttgagcctga taacccatgc 1620
64 caggtcttat agattcctga tctagaacct ttccaggcaa tctcagacct aatttccttc 1680
65 tgttctcctt gttctgttct gggccagtga aggtccttgt tctgattttg aaacgatctg 1740
66 caggtcttgc cagtgaaccc ctggacaact gaccacaccc acaaggcatc caaagtctgt 1800
67 tggtctccaa tccatttctg tgtcctgctg gaggttttaa cctagacaag gattccgctt 1860
68 attccttggg atggtgacag tgtctctcca tggcctgagc agggagatta taacagctgg 1920
69 gttcgcagga gccagccttg gccctgttgt aggcctgttc tgttgagtgg cacttgcttt 1980
70 ggggtccaccg tctgtctgct ccctagaaaa tgggctgggt cttttggccc tcttctttct 2040
71 gagggccact ttattctgag gaatacagtg agcagatatg ggcagcagcc aggtagggca 2100
72 aaggggtgaa gcgcaggcct tgctggaagg ctatttactt ccatgcttct ctttttctta 2160
73 ctctatagtg gcaacatttt aaaagctttt aacttagaga ttaggctgaa aaaaataagt 2220
74 aatggaattc acctttgcat cttttgtgtc tttcttatca tgatttggca aaatgcatca 2280
75 cctttgaaaa tatttcacat attggaaaag tgctttttaa tgtgtatatg aagcattaat 2340
76 tacttgtcac tttctttacc ctgtctcaat attttaagtg tgtgcaatta aagatcaaat 2400
77 agatacatta agagtgtgaa ggctggctctg aaggtagtga gctatctcaa tcggattgtt 2460
78 cacactcagt tacagattga actccttgtt ctacttcctt gcttctctct actgcaattg 2520
79 actagtcttt aaaaaaaagt gtgaagagta agcaataggg ataaggaaat aagatct 2577

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81 &lt;210&gt; SEQ ID NO: 2

82 &lt;211&gt; LENGTH: 357

83 &lt;212&gt; TYPE: PRT

84 &lt;213&gt; ORGANISM: Artificial Sequence

86 &lt;220&gt; FEATURE:

87 &lt;223&gt; OTHER INFORMATION: Targeting vector

89 &lt;400&gt; SEQUENCE: 2

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90 Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
91 1 5 10 15
92 Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg
93 20 25 30
94 Gln Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile
95 35 40 45
96 Val Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys
97 50 55 60
98 Thr Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile
99 65 70 75 80
100 Ala Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala
101 85 90 95
102 Ala Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser
103 100 105 110
104 Met Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile
105 115 120 125
106 Ser Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr
107 130 135 140
108 Trp Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile
109 145 150 155 160
110 Trp Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln

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```

111           165           170           175
112 Ile Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser
113           180           185           190
114 Asp Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile
115           195           200           205
116 Leu Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile
117           210           215           220
118 Ile Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala
119 225           230           235           240
120 Leu Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe
121           245           250           255
122 Pro Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met
123           260           265           270
124 Phe Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln
125           275           280           285
126 Val Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu
127           290           295           300
128 Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
129 305           310           315           320
130 Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
131           325           330           335
132 Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
133           340           345           350
134 Gly Ala Leu Ser Leu
135           355
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139 <211> LENGTH: 200
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Targeting vector
146 <400> SEQUENCE: 3
147 tattccttac agagccttat tcctggcatg tttgatgact tcagctatga ctccactgct 60
148 tccacagatg actacatgaa tttgaatttc agtagcttct tctgtaagaa aaataatgtc 120
149 aggcagtttg caagccattt tctcccacct ctgtactggc ttgtgttcat tgtgggcacc 180
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152 <210> SEQ ID NO: 4
153 <211> LENGTH: 200
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Targeting vector
160 <400> SEQUENCE: 4
161 tgtacaagat gaacttctac agctgtgtgc ttctcatcat gtgcatcagt gtggacagat 60
162 acattgccat tgtacaggcc atgaaggctc aggtctggag gcagaaaagg ccgctataca 120
163 gcaagatggc ctgcattacc atctgggtga tggcagctgt gctctgcacc ccagaaatcc 180
164 tgtacagtca agtcagtggg                                     200

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